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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
. Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US

2: /cgn2_6/ptodata/2/pubpaa/US

3: /cgn2_6/ptodata/2/pubpaa/US

4: /cgn2_6/ptodata/2/pubpaa/US

4: /cgn2_6/ptodata/2/pubpaa/US

5: /cgn2_6/ptodata/2/pubpaa/US

6: /cgn2_6/ptodata/2/pubpaa/US

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11: /cgn2_6/ptodata/2/pubpaa/US

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18: /cgn2_6/ptodata/2/pubpaa/US
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Gapop 10.0 , Gapext 0.5
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//cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
SUMMARIES
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792.077 Million cell updates/sec
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Result No.	Score	Query	Query Match Length	₽B	ID	Description
<b>_</b>	2987	99.8	566	8	US-08-813-323A-1	Sequence 1,
N	2886.5	96.4	568	œ	US-08-813-323A-2	Sequence 2,
w	2710	90.5	543	10	US-09-757-041-2	Sequence 2
4	2102.5	70.2	438	10	US-09-950-902-2	Sequence 2
ۍ.	1613	53.9	347	10	US-09-950-902-4	Sequence 4
6	204	6.8	43	10	US-09-798-789-4	Sequence 4
7	204	6.8	43	10	US-09-981-289-4	Sequence 4
80	186.5	6.2	72	10	US-09-864-761-33993	Sequence 33993,
9	150	5.0	658	10	US-09-764-864-818	Sequence 818,
10	146	4.9	563	10	US-09-764-864-1277	Sequence 1277, Ap
11	144	4.8	185	9	US-09-949-842-19	Sequence 19, Appl
12	142	4.7	232	10	US-09-998-667-1	Sequence 1, Appli
13	133.5	4.5	2053	ø	US-10-017-216-2	Sequence 2,
14	133	4.4	239	10	US-09-998-667-7	Sequence 7, Appli
15	133	4.4	1641	ø	US-10-017-216-5	Sequence 5, Appli
16	131.5	4.4	503	10	US-09-764-864-835	Sequence 835, App
17	131.5	4.4	1958	12	US-10-028-946-4	Sequence 4, Appli
18	131.5	4.4	2054	12	US-10-028-946-2	Sequence 2
19	131.5	4.4	2139	10	US-09-727-384-6	Sequence 6

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125.5 125.5 125.5 125.5 124.5 124.5 124.5 122.2 122.2 122.2 122.2 122.2 122.2 122.3 122.3 122.3 122.5 123.5 124.5 125.5 126.5 126.5 127.5 127.5 128.5 129.5	129
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285 829 412 1863 1863 1863 1863 1063 677 1138 2015 600 228 231 231 231 231 231 231 231 231 231 231	245
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US-09-764-864-861 US-09-764-865-8 US-09-734-672-2 US-09-734-672-2 US-09-734-672-6 US-09-734-672-6 US-09-745-763-168 US-09-767-215-5 US-09-767-215-5 US-09-767-215-5 US-09-767-215-5 US-09-767-215-6 US-09-764-864-837 US-09-764-864-837 US-09-764-864-808 US-09-771-161A-226 US-09-771-161A-226	US-09-998-667-9
Sequence 841, Appli Sequence 8, Appli Sequence 4, Appli Sequence 1689, App Sequence 6, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 8, Appli Sequence 1306, Ap Sequence 1306, Ap Sequence 1292, Ap Sequence 6, Appli Sequence 6, Appli Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 577, App Sequence 577, App Sequence 224, App Sequence 225, App Sequence 225, App Sequence 226, App Sequence 226, App	Sequence 9, Appli

## ALIGNMENTS

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RESULT 1
US-08-813-323A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Baltim
APPLICANT: Cheng,
                                                                                                                                               ATTORNEY/AGENT INFORMATION:

NAME: White, John P
REGISTRATION UNMBER: 28,678
REFERENCE/DOCKET NUMBER: 5065
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 278-0400
                                                    TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 566 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ye, Zheng-sheng
TITLE OF INVENTION: TRUNCATED CRAF1 INHIBITS CD40 SIGNALING
NUMBER OF SEQUENCES: 5
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1185 A
CITY: New York
STATE: New Yor
                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                    TOPOLOGY:
                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                               10036
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1185 Avenue of the Americas
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Cheng, Genhong
Cleary, Aileen
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                    linear
peptide
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; LOCATION:
US-08-813-323A-1
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                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08813323A Patent No. US20020031522A1 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                         ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                            APPLICANT: Lederman, Seth
APPLICANT: Ye, Zheng-sheng
TITLE OF INVENTION: TRUNCATED CRAF1 INHIBITS CD40 SIGNALING
NUMBER OF SEQUENCES: 5
                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            APPLICANT: Cheng, Genhong APPLICANT: Cleary, Alleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                COUNTRY:
                                                                                                 CITY: New York
STATE: New York
                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELESYDKSAGQAARNTGLLESQLSRHDQTLSYHDIRLADMDLRFQYLETASYNGYLIWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IEROKEMLRNNESKILHLORVIDSQAEKLKELDKEIRPFRONWEEADSMKSSVESLONRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREATCSHCK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREATCSHCK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPKQTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREILALQVYCRNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MESSKKMDAAGTLQPNPPLKLQPDRGAGSVLVPEQGGYKEKFVKTVEDKYKCEKCRLVLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              566;
                                                                                                   New York
                                                                                                                             E: Cooper & Dunham, LLP
1185 Avenue of the Americas
                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                               Baltimore, David
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Pred. No. 1.3e-208;
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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Relacion DATA: CURRENT APPLICATION DATA: APPLICATION NUMBER: US, FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide FEATURE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
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                                                             TVLENGTYIKDDTIFIKVIVDTSDLPDP
                                                                                                                           EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ
                                                                                                                                                                                      KIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRG
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US-09-757-041-2 ; Sequence 2, Application US/09757041 ; Patent No. US20020009726A1

GENERAL INFORMATION:

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TELEPHONE: (619) 535-9901
TELEFAX: (619) 535-9949
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/757,041
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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STATE: California
COUNTRY: USA
ZIP: 92122
                                                                                                                                                                                                            218 -- GTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEI
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1203
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                    KIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRG
                                                                                                                                                      EIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR
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4370 La Jolla Village Drive,
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Pred. No. 1.3e-188;
7; Mismatches 16;
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Best Local Similarity 72.9%;
Matches 415; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The Trustees of Columbia University in the City of TITLE OF INVENTION: TRAF-3 DELETION ISOFORMS AND USES THEREOF FILE REFERENCE: 58732-A-PCT CURRENT APPLICATION NUMBER: US/09/950,902 CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US00/06503
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/268,544
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                             VTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIW
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               GEYDALLPWPFKQKYTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVA 538
                                                            KIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVI-MR
                                                                                                                          VTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETASYNGVLIW
                                                                                                                                                                                                           EIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR
GEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVA
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Pred. No. 8.6e-145;
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US-09-950-902-4
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Patent No. US20020127615A1
GENERAL INFORMATION:
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Best Local Similarity 58.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/950,902
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/US00/06503
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/268,544
PRIOR APPLICATION NUMBER: 09/268,544
PRIOR ETILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: The Trustees of Columbia University in the TITLE OF INVENTION: TRAF-3 DELETION ISOFORMS AND USES FILE REFERENCE: 58732-A-PCT
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320
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 TVLENGTYIKDDTIFIKVIVDTSDLPDP
                                                                                           EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ
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RESULT 6

Penn, Sharron G. Rank, David R.

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GENERAL INFORMATION:
APPLICANT: Penn, Sh
APPLICANT: Rank, D
                                                                                                                                      Sequence 33993, Application US/09864761 Patent No. US20020048763A1
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APPLICANT: Dahiyat, Bassil I.
APPLICANT: Filikov, Anton
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA FOR THE TREATM
TITLE OF INVENTION: ALPHA RELATED DISORDERS
TITLE REFERENCE: A-68990-3/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS/RFT/RMS
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LENGTH: 43
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Best Local Similarity 97.6%;
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Best Local Similarity 97.6%;
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APPLICANT: Filikov, Anton
APPLICANT: Filikov, Anton
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
TITLE OF INVENTION: UNSORDERS
FILE REFERENCE: A -68990-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/798,789
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,427
PRIOR APPLICATION NUMBER: US 60/186,427
PRIOR APPLICATION NUMBER: US 60/186,427
PRIOR SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver: 2.1
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SOFTWARE: PatentIn version 3.1
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TYPE: PRT
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Pred. No. 8.3e-09;
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Pred. No. 8.3e-09;
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33993
LENGTH: 72
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PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BY474, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BY474, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 1.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                  493 VTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLEN--GTYIKD 550
                                                                                                                                Match 6.2%;
Local Similarity 51.4%;
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FILING DATE: 2001-01-07
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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VTFMLLDQ-NNREHAIDAFRPDLSSASFQRPQSETNVASGCPLFFPLSKLQSPKHAYVKD 59
                                                                                                                                                                                                                                             INFORMATION:
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                                                                                                               Conservative
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EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
EST_HUMAN HIT: AW136067.1, EVALUE 1.00e-18
SWISSPROT HIT: Q13077, EVALUE 3.00e-37
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Pred. No. 2.9e-07;
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US-09-764-864-818
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Patent No. US20020132753A1
GENERAL INFORMATION:
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US-09-764-864-1277
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
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                        GENERAL INFORMATION:
                                             Sequence 1277, Application US/09764864 Patent No. US20020132753A1
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APPLICANT: Rosen et al.
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OTHER INFORMATION:
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 FECSLCMRLFFEPVTTPCGHSFCKNCLERCL-DHAPYCPLCKESL-----KEY 408
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                                                                                                                                                                                     589 SQILQHEGSMPEREENLQAAPNGPAWCWWLLAVLPVDPRYQLSVLSMKSLKERLTKIQHI 648
                                                                                                                                                                                                                              335 E--IRPFRONWEEADSMKS------366
                                                                                                                                                                                                                                                                            537 -----RGMKDGYCT--ADIEYLEDVKVENEDEIKNLRELHDLVYSQACSWFQNLRDRFR 588
                                                                                                                                                                                                                                                                                                                       282 EKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVID---SQA----EKLKELDK 334
                                                                                                                                                                                                                                                                                                                                                                       496 SDTQN-SFADYGCMLQ------ S36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            437 KIYDEETAELSHLTKNVPIFVCTMAYPTVPCPLHVFEPRYRLMIRRSIQTG-TKQFGMCV 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 5.0%; Score 150; DB 10; Length 658; Local Similarity 19.2%; Pred. No. 0.0021; les 69; Conservative 71; Mismatches 104; Indels 11
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

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US-09-949-842-19; Sequence 19, Application US/09949842; Patent No. US20020164692A1; GENERAL INFORMATION:
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    APPLICANT: Ni et al.
TITLE OF INVENTION: PT047P1
FILE REFERENCE: Immune System-Related Polynucleotides, Polypeptides, and Antibodies CURRENT APPLICATION NUMBER: US/09/949,842
CURRENT FILLING DATE: 2001-09-02
CURRENT FILLING DATE: 2001-09-02
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PRIOR APPLICATION NUMBER: PCT/US01/07260
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CURRENT FILING DATE: 2001-01-17
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE LOCATION: (40)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE LOCATION: (6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                 477
                                                                                                                                                                                                                                                                                                                                                                                              436 SDTQN-SFADYGCMLQ------IRNVHFLPDGRSVVDTVGGKRFRVLK----
                                                                                                                                                                                                                                                                                                                                                 282 EKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVID---SQA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 KIYDEETAELSHLTKNVPIFVCTMAYPTVPCPLHVFEPRYRLMIRRSIQTG-TKQFGMCV 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 K-YREATC--SHCKSQVPM-IKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 LA------DRRYCVTQLL------------EELIVKYLPDELSERK 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 LALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKAC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 FECSLCMRLFFEPVTTPCGHSFCKNCLERCL-DHAPYCPLCKESL------KEY 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 YKCEKCRLVLCNPKQTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                    -----RGMKDGYCT--ADIEYLEDVKVENEDEIKNLRELHDLVYSQA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLE----KKVSLLQNESV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xaa equals any of the naturally occurring L-amino acids
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21.2%; Pred. No. 0.0034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 563;
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US-09-998-667-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. U.Z. Patent No. Barena I INFORMATION:
APPLICANT: Masuda, Esteban
APPLICANT: Liao, X. Charl
                                                                                                                                                            Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09998667 Patent No. US20020146747A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/998,667
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: US 60/282,432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pardo, Jorge
APPLICANT: Rigel Pharmaceutical
TITLE OF INVENTION: TRAC1: Modu
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                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2
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                                                                                                                                                                                                                                                                                             LENGTH: 232
TYPE: PRT
ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 60/224,367
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/187,873
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                       OTHER INFORMATION: human wild-type TRAC1 (FLJ20456)
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SOFTWARE: PatentIn Ver. 2.0
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TYPE: PRT
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                                   110 LALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKAC 169
                                                                                                   93 -----MKSEYKNCAE----
                                                                          35 FDCAVCLEVLHOPVRTRCGHVFCRSCIATSLKNNKWTCPYCRAYLPSEGVPATDVAKR-- 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 IFVTCITAMS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 ----CVNAPS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 KYID-----KYGPLQELEETAARCVCPFCQRELYEDSLLDHCITHHRSERRPVVR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 LALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKAC 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 YKCEKCRLVLCNPKQTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 4.8%; Score 144; DB 9; Local Similarity 23.7%; Pred. No. 0.0011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pardo, Jorge
Rigel Pharmaceuticals, Incorporated
Rigel Pharmaceuticals, Incorporated
Rigel Pharmaceuticals, Incorporated
Rigel Pharmaceuticals, Incorporated
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Chu, Peter
                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  2001-04-06
                                                                                                                                                    4.7%; Score 142; DB 10; .
24.2%; Pred. No. 0.0021;
7. Mismatches 73;
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                                                                                                                                                                                           DB 10; Length 232;
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----CDTLVCLSEMRAHIRTCQ 120
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                                                                                                                                                        Indels
                                                                                                                                                      Gaps
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US-09-998-667-7
; Sequence 7, Application US/09998667
; Patent No. US20020146747A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 2053
APPLICANT: Masuda, Esteban
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Patent No. US20020160483A1
GENERAL INFORMATION:
APPLICANT: KAPELLER-LIBERMANN, ROSANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/017,216
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 60/242,429
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 7
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TITLE OF INVENTION: Kinase and Uses Therefor
FILE REFERENCE: 10147-57U1
                                                                                                                                                                             872 SDKNRLLELETRLREVSLEHEEQKLELKR-QLTELQLSLQERES 914
                                                                                                                                                                                                                                                                      814 NKLAANSSLFTQRNNKAQEEMISELRQQKFYLETQAGKLEA-QNRKLE-EQLEKISHQDH
                                                                                                                                                                                                                         373 AARN-----TGLLESQLSRHDQTLSVHDIRLADMDLRFQVLET 410
                                                                                                                                                                                                                                                                                                                  327 EKL-----KELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQ-- 372
                                                                                                                                                                                                                                                                                                                                                                                                              276 LQNESVEKNKSIQSLHNQICSFEIE-----IERQKEMLRNNESKILHL-QRVID-SQA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                             694 MERRENRLKDDIQTKSQQIQQMADKILELEEKHREAQVSAQHLEVHLKQKEQHYEEKIKV 753
                                                                                                                                                                                                                                                                                                                                                                 754 LDNQIKKDLADKETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSEA 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 LQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKACKY 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        526 MEVSQEDDKA------LQLLHD-----IREQ-SRKLQEIKEQEYQAQVEEMRLMMN 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 CSFK--RYGCVFQGTNQ0I------KAHEASSAVQHVNL-LKEWSNSLEKKVSL 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NPKQTECGHR------FCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREILA 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 KYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPS 229
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; LENGTH: 1641
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-017-216-5
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                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: KAPELLER-LIBERMANN, ROSANA
TITLE OF INVENTION: Kinase and Uses Therefor
TITLE OF INVENTION: Kinase and Uses Therefor
FILE REFERENCE: 10147-5701
CURRENT FILING DATE: US/10/017,216
CURRENT FILING DATE: 2001-10-23
                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 5
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10017216
Patent No. US20020160483A1
                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/242,429
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 239
TYPE: PRT
ORGANISM: Mus sp.
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APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: TRACI: Modulators of Lymphocyte Activation
FILE REFERENCE: 021044-000600US
CURRENT APPLICATION NUMBER: US/09/998,667
CURRENT FILING DATE: 2001-12-03
CURRENT FILING DATE: 2001-12-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MOD_RES
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OTHER INFORMATION: Xaa = Arg or Ser
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OTHER INFORMATION: mouse TRAC1 protein (3rd frame)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 KYGPLLEL---GDTTARCVCPFCQRELDEDCLLDHCIIHHRSE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 QNCAE----- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 SQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 RGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREATCSHCK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 PVRTRCGHVFCRSCIATSIKNNNKWTCPYCRAYLPSEGVPATDIAKR-----MKSEY 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PKOTECGHRECESCMAALLSSSSP-KCTACQESIIKDKVFKDNCCKREILALQVYCRNEG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 DSSKSAPASAT-----PRTL------ERSGDSELPITS----FDCSVCLEVLHQ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 4.4%; Score 133; DB 10; Local Similarity 23.3%; Pred. No. 0.0099; les 52; Conservative 27; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ESSKKMDAAGTLQPNPPLKLQPDRGAGSVLVPEQGGYKEKFVKTVEDKYKCEKCRLVLCN 61
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Zhao, Haoran
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  4.48;
Pred. No. 0.11;
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Search completed: December 19, 2002, 15:05:39 Job time : 15 secs
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                                                                                                                                                                                                                                                                                                                                               172 QSRKLQEIKEQEYQAQVEEMRLMMNQLEED-----LVSARRRSDLYESELRESRLAA-- 223
                                                                                                                                                                                                                                                                                                                                                                                                                 128 TLGHLLVHLK-NECQ----FEELPCLRADC-----KEKVLRKD-----LRDHVE 166
                                                                                                                                      341 LKQKEQHYEEKIKVLDNQIKKDLADKESLENMMQRHEEEAHEKGKILSEQKAMINAMDSK 400
                                                                                                                                                                       318 LORVIDSQAEKLKELDKEIRP-----FRONWEEA-----DSMKSS 352
                                                                                                                                                                                                                                         274 -SILONESVEKNKS---IQSLHNQICSFE-----IEIERQKEMLRNNESKI-----LH 317
                                                                                                                                                                                                                                                                            224 EEFKRKANECOHKLMKAKDQGKPEVGEYSKLEKINAEQQLK-IQELQEKLEKAVKASTEA 282
                                                                                                                                                                                                                                                                                                            222 SECVNAPSTCSFKRYGCVFQGTNQ--QIKAHEASSAVQHVNLLKEWSNSLEKKV----- 273
                                                                                                                                                                                                                                                                                                                                                                                167 KACKYREATCSHCKSQVPMIKL---QKHEDTDCPCVVVSCPHKCSV--QTLLRSELSAHL 221
                                                                    401 IRSLEQRIVELSEANKLAANSSLFTQRNMKAQEEMIS 437
                                                                                                 353 VESLONRVTELESVDKSAGQAA----RNTGLLESQLS 385
                                                                                                                                                                                                        73 ESCMAALLSSSSPKCTACQES--IIKDKVFKDN---CCKREILALQVYCRNEGRGCAEQL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94; Conservative 64; Mismatches 137; Indels 102; Gaps
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